CLAIMS

What is claimed is:

1. An isolated nucleic acid sequence encoding a polypeptide with isoflavone synthase activity having the amino acid sequence set forth in SEQ ID NO:66 wherein

	synthase activity having the amino acid sec
5	Xaa ₁₀ is Phe or Leu
	Xaa ₁₆ is Ser or Leu
	Xaa ₂₃ is Ser or Thr
	Xaa ₂₅ is Ile or Lys
	Xaa39 is Lys or Arg
10	Xaa ₄₈ is Pro or Leu
	Xaa ₆₀ is Pro or Leu
	Xaa ₇₃ is Leu or His
	Xaa ₇₄ is Ser or Tyr
	Xaa ₉₅ is Ala or Thr
15	Xaa ₉₆ is Asn or His
	Xaa ₁₀₂ is Asn or Ser
	Xaa ₁₁₀ is Ile, Val, or Thr
	Xaa ₁₁₂ is Arg or His
	Xaa ₁₁₇ is Asn or Ser
20	Xaa ₁₁₈ is Ser or Leu
	Xaa ₁₂₁ is Met or Arg
	Xaa ₁₂₂ is Ala or Val
	Xaa ₁₂₄ is Phe or Ile
	Xaa ₁₂₉ is Lys or Arg
25	Xaa ₁₄₇ is Lys or Glu
	Xaa ₁₅₉ is Leu or Phe
	Xaa ₁₆₂ is Ala or Val
	Xaa ₁₆₆ is Ser or Gly
	Xaa ₁₇₀ is Gln or Arg
30	Xaa ₁₇₅ is Val or Leu
	Xaa ₁₈₃ is Ala or Thr
	Xaa ₁₈₇ is Thr or Ile
	Xaa ₁₉₁ is Met or Val
	Xaa ₂₀₉ is Phe or Tyr
35	Xaa ₂₁₉ is Arg or Trp
	Xaa ₂₂₃ is Tyr or His
	Xaa ₂₅₃ is Gly or Glu
	Xaa ₂₅₉ is Lys or Glu

		Xaa ₂₆₃ is Val or Asp
		Xaa ₂₆₄ is Val, Asp, or Ile
		Xaa ₂₆₈ is Ala or Val
		Xaa ₂₇₂ is Phe or Leu
	5	Xaa ₂₈₅ is Thr or Met
•		Xaa ₂₉₃ is Glu or Asp
		Xaa ₂₉₄ is Thr, or Ile
		Xaa ₃₀₁ is Phe or Leu
		Xaa ₃₀₆ is Thr or Ile
	10	Xaa ₃₁₁ is Val or Glu
ā		Xaa312 is Val or Ala
1		Xaa ₃₂₅ is Arg or Lys
w Li		Xaa ₃₂₈ is Gln or Glu
		Xaa ₃₃₄ is Val or Ala
	15	Xaa ₃₄₂ is Arg or Ile
		Xaa ₃₇₇ is Thr or Ile
: -		Xaa ₃₈₁ is Glu or Gly
		Xaa ₃₈₅ is Tyr, His, or Cys
<u> </u>		Xaa ₃₈₇ is Ile or Thr
	20	Xaa ₃₉₃ is Val or Ile
ļ.		Xaa ₃₉₄ is Leu or Pro
		Xaa ₄₀₂ is Arg or Lys
		Xaa ₄₀₄ is Ser or Pro
		Xaa ₄₁₃ is Ser or Phe
	25	Xaa ₄₂₂ is Glu or Gly
		Xaa ₄₂₈ is Gly or Arg
		Xaa ₄₂₉ is Pro or Leu
		Xaa ₄₃₅ is Gln or Arg
		Xaa ₄₄₇ is Arg or Gly
	30	Xaa ₄₅₃ is Asn, Ser, or Ile
		Xaa ₄₅₉ is Met or Thr, and
		Xaa ₄₈₅ is Asp or Gly.
r		2. An isolated polypeptide sequence of SEQ ID NO: 66 wherein
		Xaa ₁₀ is Phe or Leu
•	35	Xaa ₁₆ is Ser or Leu
		Xaa ₂₃ is Set of Thr
		Xaa ₂₅ is the or Lys
		Xaa ₃₉ is Lys or Arg
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	Xaa ₄₈ is Pro or Leu
	Xaa ₆₀ is Pro or Leu
	Xaa ₇₃ is Leu or His
	Xaa ₇₄ is\Ser or Tyr
5	Xaa ₉₅ is Ala or Thr
	Xaa ₉₆ is Asn or His
	Xaa ₁₀₂ is Asn or Ser
	Xaa ₁₁₀ is Ile, Val, or Thr
	Xaa ₁₁₂ is Arg or His
10	Xaa ₁₁₇ is Asn or Ser
	Xaa _{l 18} is Ser or leu
	Xaa ₁₂₁ is Met or Arg
CONTROL OF THE CONTRO	Xaa ₁₂₂ is Ala or Val
	Xaa ₁₂₄ is Phe or Ile
15	Xaa ₁₂₉ is Lys or Arg
	Xaa ₁₄₇ is Lys or Glu
	Xaa ₁₅₉ is Leu or Phe
15 15 15 20	Xaa ₁₆₂ is Ala or Val
	Xaa ₁₆₆ is Ser or Gly
2 0	Xaa ₁₇₀ is Gln or Arg
	Xaa ₁₇₅ is Val or Leu
	Xaa ₁₈₃ is Ala or Thr
E.	Xaa ₁₈₇ is Thr or Ile
	Xaa ₁₉₁ is Met or Val
25	Xaa ₂₀₉ is Phe or Tyr
	Xaa ₂₁₉ is Arg or Tr
	Xaa ₂₂₃ is Tyr or His
	Xaa ₂₅₃ is Gly or Glu
	Xaa ₂₅₉ is Lys or Gly
30	Xaa ₂₆₃ is Val or Asp
	Xaa ₂₆₄ is Val, Asp, or Ile
	Xaa ₂₆₈ is Ala or Val
	Xaa ₂₇₂ is Phe or Leu
	Xaa ₂₈₅ is Thr or Met
35	Xaa ₂₉₃ is Glu or Asp
	Xaa ₂₉₄ is Thr, or Ile
	Xaa ₃₀₁ is Phe or Leu
	Xaa ₃₀₆ is Thr or Ile
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Xaa₃ is Val or Glu Xaa_{3 l} is Val or Ala Xaa₃₂ is Arg or Lys Xaa₃₂₈\is Gln or Glu Xaa334 is Val or Ala Xaa342 is Arg or Ile Xaa₃₇₇ is Thr or He Xaa₃₈₁ is Glu or Gly Xaa₃₈₅ is Tyr, His, or Cys Xaa387 is Ile or Thr Xaa393 is Val or Ile Xaa394 is Let or Pro Xaa₄₀₂ is Arg or Lys Xaa₄₀₄ is Ser or Pro Xaa413 is Ser dr Phe Xaa422 is Glu or Gly Xaa₄₂₈ is Gly/of Arg Xaa₄₂₉ is Pro or Leu Xaa₄₃₅ is Gln or Arg Xaa₄₄₇ is Arg or Gly Xaa453 is Asn, Ser, or Ile Xaa459 is Met or Thr, and Xaa₄₈₅ is Asp or Gly.

- An isolated nucleic acid sequence encoding a polypeptide with isoflavone
 synthase activity.
 - 4. An isolated nucleic acid sequence encoding a polypeptide with isoflavone synthase activity wherein the nucleic acid sequence is not the nucleic acid sequence set forth in SEQ ID NO:9.
 - 5. The isolated nucleic acid sequence of Claim 1 at least 85% identical to the nucleic acid set forth in SEQ ID NO:1.
 - 6. The isolated nucleic acid equence of Claim 1 at least 90% identical to the nucleic acid set forth in SEQ ID NO:1.
 - 7. The isolated nucleic acid sequence of Claim 1 wherein the nucleic acid hybridizes to the nucleic acid set forth in SEQ ID NO:1
 - 8. The isolated nucleic acid sequence of Claim 1 wherein the encoded polypeptide comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO:2.

9. The isolated nucleic acid sequence of Claim 1 selected from the group consisting of SEQ ID NOs:1, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 47, 54, 56, 58, and 60.

- 10. The isolated nucleic acid sequence of Claim 1 encoding the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NOs:2. 10, 16. 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 48, 55, 57, 59, 61, and 66.
- 11. A chimeric sequence comprising the nucleic acid sequence of Claim 1 operably linked to suitable regulatory sequences.
 - 12. A transformed host cell comprising the chimeric sequence of Claim 11.
- 13. The transformed host cell of Claim 12 further comprising a second chimeric sequence comprising a nucleic acid sequence encoding a polypeptide that regulates expression of at least one enzyme of the phenylpropanoid pathway.
- 14. The transformed host cell of Claim 13 wherein the second chimeric sequence comprises a chimera containing the maize R region between the region encoding the C1 DNA binding domain and the C1 activation domain.
 - 15. The transformed host cell of Claim 12 wherein the host cell is a eukaryotic cell.
 - 16. The eukaryotic cell of Claim 13 wherein the cell is a yeast cell.
 - 17. The eukaryotic cell of Claim 15 wherein the cell is a plant cell.
 - 18. The plant cell of Claim 17 wherein the cell is a soybean cell.
 - 19. The plant cell of Claim 17 wherein the cell is a corn cell.
 - 20. A plant comprising in its genome the chimeric sequence of Claim 11.
- 21. The plant of Claim 20 further comprising in its genome a second chimeric sequence comprising a nucleic acid sequence encoding a polypeptide that regulates expression of at least one enzyme of the phenylpropanoid pathway.
 - 22. The plant of claim) 20 wherein the plant is a soybean plant.
 - 23. The plant of claim 20 wherein the plant is a corn plant.
 - 24. A seed from the plant of Claim 20.

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- 25. A seed from the plant of Claim 21.
- 26. A method of altering the level of expression of isoflavone synthase in a host cell comprising:
 - (a) transforming a host cell with the chimeric sequence of Claim 11;
 - (b) optionally transforming the host cell with a second chimeric sequence comprising a nucleic acid sequence encoding a polypeptide that regulates expression of at least one enzyme of the phenylpropanoid pathway; and
 - (c) growing the transformed host cell produced in step (a) or step (b) under conditions that are suitable for expression of the chimeric sequence

- 27. A method of increasing the amount of an isoflavonoid in a host cell comprising:
 - (a) transforming a host cell with the chimeric sequence of Claim 11:
 - (b) optionally transforming the host cell with a second chimeric sequence comprising a nucleic acid sequence encoding a polypeptide that regulates expression of at least one enzyme of the phenylpropanoid pathway; and
- (c) growing the transformed host cell produced in step (a) or step (b) under conditions that are suitable for expression of the chimeric sequence wherein expression of the chimeric sequences results in production of an amount of an isoflavonoid in the transformed host cell that is greater than the amount of the isoflavonoid that is produced in a cell that is not transformed with the chimeric sequence of Claim 11.
- 28. The method of Claim 26 wherein the isoflavonoid is selected from the group consisting of genestein and daidzein.
 - 29. The method of Claim 26 or Claim 27 wherein the host cell is a eukaryotic cell.
 - 30. The method of Claim 26 or Claim 27 wherein the eukaryotic cell is a yeast cell.
 - 31. The method of Claim 26 or Claim 27 wherein the eukaryotic cell is a plant cell.
 - 32. The method of Claim 31 wherein the plant cell is a soybean cell.
 - 33. The method of Claim 31 wherein the plant cell is a corn cell.
 - 34. A method of producing a plant with increased isoflavonoid content comprising
 - (a) transforming a plant cell with the chimeric sequence of Claim 11;
 - (b) optionally transforming the plant cell with a second chimeric sequence comprising a nucleic acid sequence encoding a polypeptide that regulates expression of at least one enzyme of the phenylpropanoid pathway; and
 - (c) growing the transformed plant cell under conditions that promote the regeneration of a whole plant from the transformed cell
- wherein the transformed plant regenerated from the transformed cell produces an amount of an isoflavonoid that is greater than the amount of the isoflavonoid that is produced in a plant that is regenerated from a plant cell that is not transformed with the chimeric sequence of Claim 11.
 - 35. The method of Claim 34 wherein the plant is a soybean plant.
 - 36. The method of Claim 34 wherein the plant is a corn plant.
 - 37. The transgenic plant produced by the method of Claim 34.
 - 38. The transgenic plant of Claim 37 wherein the plant is a soybean plant.
 - 39. The transgenic plant of Claim 37 wherein the plant is a corn plant.

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- 40. A seed from the plant of Claim 37.
- 41. A method of obtaining a nucleic acid sequence encoding all or a substantial portion of the amino acid sequence encoding a plant isoflavone synthase comprising
 - (a) probing a cDNA or genomic library with the nucleic acid sequence of Claim 1:
 - (b) identifying a DNA clone that hybridizes with the nucleic acid sequence of Claim 1;
 - (c) isolating the DNA clone identified in step (b);
 - (d) sequencing the cDNA or genomic sequence that comprises the clone isolated in step (c); and
- (e) demonstrating the functional expression of isoflavone synthase mediated by the cDNA or genomic sequence sequenced in step (d) wherein the sequenced nucleic acid sequence encodes all or a substantial portion of the amino acid sequence encoding a plant isoflavone biosynthetic enzyme.
- 42. A method of obtaining a nucleic acid sequence encoding all or a substantial portion of an amino acid sequence encoding a plant isoflavone synthase comprising:
 - (a) synthesizing an oligonucleotide primer corresponding to a portion of the sequence set forth in a member of selected from the group consisting of SEQ ID NOs:1, 9, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 47, 34, 56, 58, and 60;
 - (b) amplifying a cDNA insert present in a cloning vector using the oligonucleotide primer of step (a) and a primer representing sequences of the cloning vector to produce an amplified nucleic acid sequence; and
- (c) demonstrating the functional expression of isoflavone synthase mediated by the amplified nucleic acid sequence produced in step (b) wherein the amplified nucleic acid sequence encodes all or a substantial portion of an amino acid sequence encoding a plant isoflavone synthase.
- 43. The method of Claim 42 wherin the oligonucleotide primer is selected from the group consisting of SEQ ID NOs:5, 6, 7, 8, 11, 12, 13, 14, 41, 42, 49, 50, and 51.
 - 44. The product of the method of Claim 41.
 - 45. The product of the method of Claim 42.
- 46. A method of altering the level of isoflavonoids in a cell of Claim 12 comprising exposing said cell to a phenylpropanoid pathway altering agent.
- 47. The method of claim 46 wherein said agent is selected from the group consisting of a transcription factor and stress.
- 48. The method of Chim 47 wherein stress is selected from the group consisting of ultraviolet light, temperature, pressure, and phosphate level.

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- 49. The method of Claim 47 wherein said transcription factor is a maize C1 myb-type transcription factor and a myc-type transcription factor R
- 50. The method of Clark 47 wherein said transcription factor is a chimera containg the maize R region between the C1 DNA binding domain and the C1 activation domain.